```
Result
No.
                                                                                                                                                                                                                                                                                                                      Minimum I
Maximum I
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                             Run
                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - protein search, using sw model
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                       DB
DB
seg length: 0 seg length: 2000000000
                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                              %
Query
BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                            US-09-331-631A-5_COPY_33_75
248
                                                                                                                                                                                                                                                                                SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                     88757 seqs, 32294092 residues
                                                                                                                                                                                                                                                                                                                                                                                                                            March 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                     NQEDPQTECQQCQRRCRQQE.....RQQQYCQRRCKEICEEEEEY
                                                                                                                                                                                                                        Length
2001, 16:16:47; Search time 91.75 Seconds (without alignments) 15.135 Million cell updates/sec
                                                                                                                                                                                                                        DB
                                                                           Y192_HUMAN
GLCX_SOYBN
TRHY_RABIT
CAS2_CAPHI
                                      GLCA_SOYBN
DHP1_SCHPO
YQEH_ECOLI
                                                         BTD_DROME
NTC3_MOUSE
FSA_HUMAN
                                                                                                                       AH12_ARAHY
CAS2_SHEEP
APA4_MACFA
ANDR_CANFA
                                                                                                    INVO_CANFA
AH11_ARAHY
YM38_YEAST
                                                                                                                                                 ANDR_HUMAN
KAPC_DICDI
ANDR_PANTR
HSP1_MOUSE
HSP1_RAT
                                                                                                                                                                                 VCLB_GOSHI
VCLA_GOSHI
AGRP_LUFCY
YS51_CAEEL
MBP1_MAIZE
TPM1_RAT
TPM2_HUMAN
TPMB_HUMAN
TPMB_RABIT
                         TRHY_HUMAN
                                                                                                                                                                                                                        ID
                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ltd
                                                                                                                                                                                                                                                                                                                                          88757
            P56568
P09662
P28794
P10275
P102779
P102319
P02319
P04654
P04654
P04654
P118174
P118174
P11827
P03825
P04883
P046841
P046841
P063883
                                                                                                                                                                                                   P09801
                                                                                                                                                                                                                       Description
                                                             1 macaca fasc
0 canis famil
4 canis famil
7 arachis hyp
5 saccharomyc
4 homo sapien
7 glycine max
9 cryctolagus
9 capra hircu
6 drosophila
mus musculu
                                                                                                                                                                   8 luffa cylin
2 caenorhabdi
4 zea mays (m
5 homo sapien
9 dictyosteli
    homo sapien
sqlycine max
schizosacch
escherichia
homo sapien
dictyosteli
rattus norv
homo sapien
homo sapien
                                                                                                                                                                                             gossypium
gossypium
luffa cyli
                                                                                                                                    arachis hypovis aries
                                                                                                                                                       pan troglod
mus musculu
                                                                                                                                                  rattus norv
                                                                                                                                           hyp
```

RESULT VCLA_G ID V	ОУ	Que Bes Mat	DR DR DR DR SQ	88888888	8888	CC CC RT RA	R O C C C C C C C C C C C C C C C C C C			
	3 81	ry t I	EMBL; PIR; A HSSP; INTERP PFAM; Seed s SIGNAL CHAIN SEQUEN	This betw the use modi enti	<del>-</del>	SEQUE Chlan "Deve- germing the single Plant -!- FI	01-1 01-1 15-0 VIC Goss Euka Magr	SULT LB_GOSH VCLB P098		4 4 4 4 4 4 3 3 3 5 5 4 4 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6
T 2 GOSHI VCLA_GOSHI	EDPQTECQQCQRCRQQESDPR	atch cal Simi 19;	M16 A308 P50, PRO; PFO Stora L	SW een by by fie fie		C.A C.A C.A C.A lopm hati tora Mol UNCT	01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence upda 15-JUL-1999 (Rel. 38, Last annotation up VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B) Gossypium hirsutum (Upland cotton). Eukaryota; Viridiplantae; Embryophyta; '1 Magnoliophyta; eudicotyledons; core eudi Malvales; Malvaceae; Gossypium. [1]	1 HI B_GOSHI BO1:		555.5555555555555555555555555555555555
STAR	QQCQRR( ::  :   EECQQE(	larity Conserv	891; AAA330 38; FW(NAB. 477; 1CAX. IPRO01113; 0546; Seeds age protein 26 5	the Swiss opean Bioinf non-profit d and this s s requires a an email to	TY: TO	FROM N.A, Pyle J ental bio on. XVIII ge protei ge protei 1. Biol. 7	(Rel. (Rel. (Rel. (Rel. PRECUR. PRECUR. rsidip a; eud lvacea	STA		2222222 222222 200.00000000000000000000
STANDARD;	QRRCRQQESD  :       QQECRQQEE-	42.3 47.5 ative	71.1  tore ; Si 25 88 88 6972	itry is co institut iformatics t instit statement a license co license	TO OTHER 7S CONGLYCININ,	A.  J.B., Le iochemist II. cDNA ein famil 7:475-48 ED STORAG LOCATION:	10, Created) 10, Last sequ 38, Last anno 38, Last anno SOR (ALPHA-GL (Upland cott lantae; Embry licotyledons; icotyledons;	NDARD;		239 524 771 771 174 174 284 284 284 284 303 441 339
	-RQ	de de	7s; nal	cop ccs itu itu int ise	7s	Legocl stry ( A and hilies 489(1) NAGE PI	eate st s pha pha don edon			
PRT;	PRQQQYCQRRCKE   :  :  :  RQRPQCQQRCLK	Score Pred. 9; Mi	1. VICILIN C:	y is copyright. It is productinstitute of Bioinformatics or institute. There are institutions as long as it atement is not removed. Usalicense agreement (See http://license@isb-sib.ch).	SEED S ETC.)	DO no	equence nnotation-GLOBULE cotton). bryophy s; core	PRT;	ALI	CALD_MELGA SBP_SOYBN CALD_CHICK HSP1_PIG GRPE_METTH TPM1_CHICK TPM1_CHICK DROME TPMB_CHICK BNK_DROME PPAS_HUMAN SRF_DROME
605	× 6	ore 105; ed. No. 0. Mismatche	2972	nt. It is particular in the state of the sta	TORAGE	Du nse cid	e update ion upda LIN B). yta; Tra e eudico	588	ALIGNMENTS	YBN HICK IG ETTH HICK OUSE OUSE OME OME OMAN OME OME
AA.		DB 1; 00057 s 1	?. ABBADE	matics There g as red. U see htt	PROTE	e L. d emb seque	update) n update) N B). a; Tracheophyta; eudicots; Rosidae	AA.	, ω	
	42 118	Length ; 0; Inde	B CRC6	ed tand and s cc	, 0	III; ryogene nces of	phyta; Rosida			
		ngth 588 Indels	4.	the res	(PHASEOL	is a	Spermatophyta e; eurosids II			P13505 Q04672 Q04672 P12957 P04101 Q27350 P04267 P46901 P16901 P193181 Q03181 P20226 Q24535
		2;		h a c EMBL trict is is nd fo -sib.	IN,	member	nato			
				colla L outs ctions s in for col b.ch/a	VIC	Η.	phyt ds I			meleagr glycine gallus sus scr methano gallus mus gallus drosoph homo sa drosoph
		Gaps		tat on no nno	ILIN,	's of	H			מט ש בעעב
		1;				~				is g max gall ofa bact bact culu culu culu fila fila pien pien

```
RESULT 3
AGRP_LUFCY
ID AGRP_LUFCY
                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 14
                                                                                                                                                                                                              P56568;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
6.5 KDA ARGININE/GLUTAMATE-RICH POLYPEPTIDE (6.5K-AGRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlan C.A., Borroto K., Kamalay J.A., Dure "Developmental blochemistry of cottonseed germination. XIX. Sequences and genomic or globulin (vicilin) genes of cottonseed."; Plant Mol. Biol. 9:533-546(1987).
Kimura M., Park S.S., Sakai R., Yamasaki N., Funatsu G.;
"Primary structure of 6.5k-arginine/glutamate-rich polypep
the seeds of sponge gourd (Luffa cylindrica) ";
Biosci. Biotechnol. Biochem. 61:984-988(1997)
-!- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND
RESERVES DURING GERMINATION AND SEEDLING GROWTH.
-!- WASS SPECTROMETRY: MW=5693.39; METHOD=WALDI.
                                                                                                                         TISSUE=SEED;
                                                                                                                                                                   Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb·sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sj
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P09799;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seed storage protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M19378; AAA33069.1; PIR; S06398; S06398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                       MEDLINE=97357433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malvales;
                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: TO OTHER 7S SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BODIES
                                                                                                                                                                                                                                                                                                                                                                                                         QEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                           QQQPDKQFKECQQRCQWQEQRPERKQQCVKECREQYQED 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P50477; 1CAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001113; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malvaceae; Gossypium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                        PubMed=9214759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605
71049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.9%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VICILIN GC72-A.; C9DB9371C976953B CRC64;
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y J.A., Dure L. III;
cottonseed embryogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STORAGE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ormatics and the EMBL outstat.
There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.0074;
                                                                                                                                                                                                                                                                                                      Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHASEOLIN, VICILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                           polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta;
e; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       its
                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
RESULT 5
MBP1_MAIZE
ID MBP1_M
AC P28794
DT 01-DEC-
DT 01-DEC-
                                                                                                                                                                               RESULT
YS51_C/
ID YS
                                                                                   В
                                                                                                     γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 13
                                                                                                                                      Query Match
Best Local
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed storage protein.
DISULFID 12 33
DISULFID 16 29
SEQUENCE 47 AA; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YS51_CAEEL
MBP1_MAIZE
P28794;
01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. : 15-JUL-1998 (Rel. : 15-JUL-1999 (Rel. : 15-JUL-1999 (Rel. : 15.6 |
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  Hypothetical protein; SIGNAL 1 1
                                                                                                                                                                                                                                                                                                                                                                   Jones S.J.M.;
Submitted (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q09662;
01-NOV-1995
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                      WORMPEP;
                                                                                                                                                                                                                                         EMBL; Z48585; CAA88486.1; -.
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                 McMurray
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZK673.
                                                                                                                                                                                                                                 HSSP; P01551;
                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 37.
                                                                                                     3 EDPOTECOOCORRCROQESDPROQOYCORRC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ģ
                                                                                                                                                                                                                                                                                                                                                C03G6.13
                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: SOME, TO
                                                                                  DDPNTDCTQYTSLCSNAKYTPLLQQFCPKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRTEYEACRVRCQVAEHGVER----QRRCQQVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTECOOCORRCROQESDPROQOYCORRCKEICEE
                                                                                                                          l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                       ZK673.1;
                                                                                                                                                                                                                                                                                                                                                                                                                      (MAR-1995)
                                                                                                                                                                               154 AA;
(Rel.
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae;
                                                                                                                                                                                        20
                                                                                                                                                                                                                                 1ACX.
                                                                                                                                                                                                                                                                                                                                                                                        N2;
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                      CE16742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,
36,
38,
KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                    27.4%;
                                                                                                                                                                              15637 MW;
                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%;
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
Last annotation
PROTEIN ZK673.1
          Created)
                                                                                                                                                                                                          signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases. TO C.ELEGANS E04D5.4 AND SOME, 1
                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 S
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB Pred. No. 0.18 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEED
                                                                                                                          Pred. No. 0.9
                                                                                                                                              Score 68;
                                                                                                                                                                                        POTENTIAL.
HYPOTHETICAL PROTEIN ZK673.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588B0EC82273AC05
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                               323A02C3A2E782AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STORAGE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                               33
                                                                                                                                                DВ
                                                                                                                                      . 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>3</u>5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 18;
                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditida; Rhabditoidea;
                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64
                                                                                                                                               Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 47;
                                                                                                                                                                               CRC64;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               II PRECURSOR
                                                                                                                                                                                                                                                                                                                                                          TO C. ELEGANS
                                                                                                                                                                                                                                                                                                                 EMBL
                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                 collaboration
L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caps
                                                                                                                          Gaps
                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲.
```

Last sequence

update)

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989
01-APR-1990
01-OCT-2000
                  SEQUENCE FROM N.A.
TISSUE=PROSTATE;
MEDLINE=89017168; PubMed=3174628;
                                                                                                                                                                                                                                    Mol.
  Chang C., K
                                                                                                                                                                      Lubahn D.B., Brown T.R., Sime Wilson E.M., French F.S.; "Sequence of the intron/exon
                                                                                                                                                                                                                                                        MEDLINE-89112008; PubMed-3216866;
Lubahn D.B., Joseph D.R., Sar M., Tan J., Hi
French F.S., Wilson E.M.;
"The human androgen receptor: complementary
                                                                                                                                                                                                                                                                                                                                                                                                            ANDR_HUMAN P10275;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                              "Specific region in hormone binding dobinding and trans-activation by human Mol. Endocrinol. 4:417-427(1990).
                                                                                                                                       "Sequence of the intron/exon junctions of the coding human androgen receptor gene and identification of in a famility with complete androgen insensitivity." Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).
                                                                                                                                                                                           MEDLINE=90083302; PubMed=2594783; Lubahn D.B., Brown T.R., Simental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungicide;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. B73; TISSUE-SEED; MEDLINE-92406801; PubMed-1527010; Duvick J.P., Rood T., Rao A.G., M
                                                                                               Govindan M.V.;
                                                                                                         MEDLINE=90258935;
                                                                                                                    SEQUENCE FROM N
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                cloning, sequence
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                  ANDROGEN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIZEDB; 69182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from maize (Zea mays L.) kernels.";
J. Biol. Chem. 267:18814-18820(1992).
-!- FUNCTION: INHIBITOR OF BOTH BACTERIAL
-!- TISSUE SPECIFICITY: PREDOMINANTLY IN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnoliophyta;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays (Maize).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, ANTIMICROBIAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                        OR NR3C4 OR DHTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                    ing, sequence analysis and gene expression Endocrinol. 2:1265-1275(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCQRRC-RQQESDPRQQQYCQRRCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A41822; A41822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECRRQCLRRHEGQPWETQECMRRCR
            С.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
 Kokontis J., lal analysis of
                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibiotic.
33 AA; 4131
                                                                                                                                                                                                                                                                                                                                                                           (Rel. 10, Created)
(Rel. 14, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                    >
                                                                                                         PubMed=2342476;
                                                                                                                                                                                                                                                                                                                                                                  (DIHYDROTESTOSTERONE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                 10, Created)
                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation MBP-1.
            Liao
complementary DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X
V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta; Spermatophyta;
; Poales; Poaceae; Zea.
            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65.5; D
Pred. No. 0.49
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B148F1B90E823599
                                                                                                                                                                                                                                                                                                                        Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marshak
                                                                                                                                                                                           J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.5;
No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                            update)
on update)
                                                                                   domain is
                                                                                                                                                                                                                                                                                                                                                                                                                       919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                         androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.R.;
                                                                                                                                                                                          Higgs H.N.,
                                                                                                                                                                                                                                                                                                                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
.49;
 and
                                                                                                                                                           the coding cation of a
                                                                                                                                                                                                                                                                             Higgs H.N.,
                                                                                                                                                                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                deoxyribonucleic
                                                                        s essential
en receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBRYO
 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNGAL
                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                              prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PORTION
acid
                                                                                                                                                                                          Migeon
                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                            point mutation
                                                                                                                                                                      region of the
                                                                                                                                                                                                                                                                              Larson
                                                                                   for
sequences
                                                                                                                                                                                           C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                    hormone
                                                                                                                                                                                                                                                        acid
                                                                                                                                                                                                                                                                              R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 of
```

```
MEDLINE=95023089; PubMed=7937057;
Patterson M.N., Hughes L.A., Gottlieb
"The androgen receptor gene mutations
Nucleic Acids Res. 22:3560-3562(1994).
                                                                                                                                                                           "Androgen receptor gene muscular atrophy."; Nature 352:77-79(1991).
                                                                                                                                                                                                                                                                                                                        Sleddens H.F., Oostra
"Trinucleotide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 468-919 FROM N.A.
MEDLINE=88240407: PubMed=3377788;
Trapman J., Klaassen P., Kuiper G.G.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 189-919 FROM N.A. MEDLINE=88178111; PubMed=3353726; Chang C., Kokontis J., Liao S.; "Molecular cloning of human and ri androgen receptors."; Science 240:324-326(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOL.
           MEDLINE=91083633; PubMed=2260966;
Veldscholte J., Ris-Stalpers C.,
                                                                       Gottlieb
                                                                                                                                                                                                         MEDLINE=91287825; Pubm
la Spada A.R., Wilson
                                                                                                                                                                                                                                                 Lu J., Danielsen M.;
Submitted (FEB-1995)
                                                                                                                                                                                                                                                                       TISSUE=BLOOD
                                                                                                                                                                                                                                                                                                                                                                                               Mulder E., Brinkmann A.O.; "Cloning, structure and ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         termination of the receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=PROSTATE;
MEDLINE=89098909; PubMed=2911578;
Marcelli M., Wilson
                                                    Nucleic
                                                                                                                                                         REVIEW ON VARIANTS.
                                                                                                                                                                                                                               VARIANTS SBMA
                                                                                                                                                                                                                                                                                                      Nucleic Acids
                                                                                                                                                                                                                                                                                                                                            MEDLINE=92220629; PubMed=1561105
                                                                                                                                                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                                                      androgen
                                                                                                                                                                                                                                                                                                                                                                                                                   Faber P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 468-919 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete androgen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPhaul M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marcelli M., Tilley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91155943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc.
                                 /ARIANT LNCAP
                                                                                  MEDLINE=97169385;
                                                                                              REVIEW
                                                                                                                                                                                                                                                                                                                (AR)
                                                                                                                                                                                                                                                                                                                                                        POLYMORPHISM OF POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Definition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl.
                                                                                            ON VARIANTS
                                                    Acids
                                                  B., Trifiro M., Lumbroso R., rogen receptor gene mutations Acids Res. 25:158-162(1997).
                                                                                                                                                                                                                                                                                                                                                                           Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                      receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat androgen receptors.";
l. Acad. Sci. U.S.A. 85:7211-7215(1988).
  C.,
                                                                                                                                                                                                                                                                                                                                                                                                                 van Rooij H.C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acad.
                                                                                                                                                                                                                                                                                 OF.
                                ALA-877
                                                                                                                                                                                                                              IN POLY-GLN
                                                                                                                                                                                                                                                                                                      Res.
  Claassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of mutations
                                                                                                                                                                                                                                                                                 POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4:1105-1116(1990).
                                                                                  PubMed=9016528;
                                                                                                                                                                                                PubMed=2062380;
lson E.M., Lubahn
r gene mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2293020;
ey W.D., Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                    20:1427-1427(1992).
                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                        B.A., Brinkmann polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M., Wilson expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ⊂
  E .
                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                               expression
                                                                                                                                                                                                                                                                                                                                                      REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              androgen receptor gene ons that cause androgen tor protein at amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                 REGION
                                                                                                                                                                                                                               REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          À
 š C., Kuiper G.G.,
van Rooij H.C.J.,
                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                   Geurts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86:327-331(1989).
                                                                                                                                                                                                                                                                                                                                                                           153:241-248(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.D.,
of a
                                                                                                                                                                                                n D
in
                                                                                                                                                                                                                                                                                                                                                                                               of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary
                                                                                                                                                                                              .B., Harding A.E., X-linked spinal a
                                                                                                                                                                                                                                                                                                                                                                                                                   van
                                                              Vasiliou database.
                                                                                                                          database
                                                                                                                                                                                                                                                                                                                        A.O.,
the a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , McPhaul
                                                                                                                                     В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffin J.E.,
                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                 , van der Korput J.A.G.M., Kessel A., Voorhorst M.M.
                                                                                                                           Pinsky
abase.";
                                                                                                                                                                                                                                                                                                                        androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haul M.J.;
encoding
                                                                                                                                                                                                                                                                                                                               Trapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gen resistance: pr
acid residue 588
                                                                                                                                                                                                                                                  databases
Trapman
           Jenster
                                                              structure permits
                                                                                                                                  ۲.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                         receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                 and
                                                                       Pinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson J.D.,
 ٩.,
                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding
                                                                                                                                                                                                        Fischbeck K.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human androgen
                                                                                                                                                                                                bulbar
                                                                      ۲.;
                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        premature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                causes
```

```
MEDLINE-9222955; PubMed=1562539; Veldscholte J., Berrevoets C.A., Ris Stalpers C., Kuiper G.G., Jenster G., Trapman J., Brinkmann A.O., Mulder E.; The androgen receptor in LNCaP cells contains a mutation in the ligand binding domain which affects steroid binding characteristic
                                                      MEDLINE=93372806; PubMed=8103398;
Lobaccaro J.-M., Lumbroso S., Ktari R.,
                                                                                                                Newmark J.R., Hardy D.O., Tonb D.C., Carter B.S., Epstein J.L Isaacs W.B., Brown T.R., Barrack E.R.; "Androgen receptor gene mutations in human prostate cancer."; Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).
                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                "A single amino acid substitution (Met-786-->Val) in the steroid-binding domain of human androgen receptor leads to complete andro insensitivity syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92235226; PubMed=1569163;
Nakao R., Haji M., Yanase T., Ogo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subjects with androgen insensitivity syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Batch J.A., williams D.M., Davies H.R., Brown Hughes I.A., Patterson M.N.;
"Androgen receptor gene mutations identified "Androgen receptor gene mutations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT CAIS ASN-695 AND HIS-695, AND SEQUE MEDLINE=92131007; PubMed=1775137; Ris-Stalpers C., Trifiro M.A., Kulper G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Androgen resistance associated with a mutation of the androgen receptor at amino acid 772 (Arg-->Cys) results from a combination decreased messenger ribonucleic acid levels and impairment of receptor function.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT CAIS METTOUV.
MEDLINE=91186983; PubMed=2082179;
Milson E.M.,
                         receptor gene of
                                                                                      VARIANT
                                                                                                                                                          Newmark J.R.,
                                                                                                                                                                            MEDLINE=92335289;
                                                                                                                                                                                                                                                                                                                          VARIANT LNCAP ALA-877
                                                                                                                                                                                                                                                                                                                                                                                                               Fukumaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT CAIS VAL-787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93338440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91310758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors from
                                                                                                                                                                                        VARIANT MET-730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS CAIS AND PAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sai T., van Rooij H.C., Kaufman M., Rosenfield R.L., Liao S.; "Substitution of asparttc acid-686 by histidine or asparagine in the human androgen receptor leads to a functionally inactive protein with altered hormone-binding characteristics."; mol. Endocrinol. 5:1562-1569(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marcelli M., Tilley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functiona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                            exonic
                                                                                                                                                                                                                                 response
   Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moi. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinol.
                                                                                     CAIS VAL-754.
                                                                                                                                                                                                                                                                                                                                                       Endocrinol. Metab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrinol. Metab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ion in the ligand binding CaP cells affects steroid to anti-androgens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function
Genet.
                                       point
                                                                                                                                                                                                                     se to antiandrogens."
Biochem. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               characterization of naturally
                                                                                                                                                                                                                                                                                                                                                                                                               Nawata H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subjects with comple
1. 4:1759-1772(1990).
             mutation creates a MaeIII site in a family with complete androgen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1:497-503(1992).
                                                                                                                                                                          PubMed=1631125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=1307250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1856263;
ey W.D., Zoppi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commun. 173:534-540(1990).
                                                                                                                                                                                                                    Biol. 41:665-669(1992).
                                                                                                                                                                                                                                                                                                                                                       74:1152-1157(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73:318-325(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete
                                                                                                                                                                                                                                                                                                                                                                                                                            Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain of the androgen receptor of binding characteristics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  androgen
                                                                                                                                                                                                                                                                                                                                                                                                                          Takayanagi R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            French
                            androgen insensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             occurring mutant androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.Е.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jenster G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F.S., Migeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insensitivity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSCP
                                                        Sultan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629-723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson
                                          the
                                                                                                                                                                                                                                                  characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans B.A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Katsube
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in
                                         an C.;
androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fourteen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Romalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            С.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
.
                                                                                                                                                                                                                                                                                                                                                                                 androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0f
```

```
RESULT 7
KAPC_DICDI
ID KAPC_DICDI
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---y-e-base substitution in exon 6 of the androgen receptor gene causing complete androgen insensitivity: the mutated receptor fails to transactivate but binds to DNA in vitro.";

Hum. Mol. Genet. 2:1809-1812(1993).
                                                      This
                                                                                                                                                                                                                         Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; "DdPK3, which plays essential roles during Dictyostelium encodes the catalytic subunit of CAMP-dependent protein Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
                                                                                                                                                                                                                                                                                                                                                      "An unusual catalytic subunit for of Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
MEDLINE=93385090; PubMed=8373760;
Anjard C., Etchebehere L., Pinaud
                                                                                                                                                                                                                                                                                                                                                                                                                                         Buerki E., Anjard C., Scholder J.-C., Reymond C.D. "Isolation of two genes encoding putative protein during Dictyostelium discoideum development."; Gene 102:57-65(1991).
                                                                                                                                                                                                                                                                                                    STRAIN=AX3
                                                                                                                                                                                                                                                                                                                                          Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=91323730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAMP-DEPENDENT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel.
01-FEB-1994 (Rel.
30-MAY-2000 (Rel.
                                        between
                                                                                                                      -I- FUNCTION: ESSENTIAL FOR DIFFERENTIATION AND FRUIT MORPHOGENESIS.
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
-I- SUBUNIT: IN DICTYOSTELLUM THE HOLDENZYME IS A DIMER COMPOSED OF A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT: IN THE PRESENCE OF CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
-I- DEVELOPMENTAL STAGE: CAPK ACTIVITY IS LOW IN VEGETATIVELY GROWIN AMOSEBAE, INCREASES DURING DEVELOPMENT OF AGGREGATION AND REACHES
                                                                                                                                                                                                                                                                                MEDLINE=93066311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKAC OR PK2 OR PK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P34099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93315568; PubMed=8325932;
Nakao R., Yanase T., Sakai Y., Ha
Nakao Raingla amino acid substitution
"A single amino acid substitution
binding domain of the human andro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [23]
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT PAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                      s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                              A MAXIMUM AS
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQQQQQQQQQQQQQQQETSPRQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEDPQTECQQCQRRCRQQESDPRQQQYCQ
                                                                                              MAXIMUM AT CULMINATION. IMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAIS ARG-807
                                                                                 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                          32:9532-9538(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                PubMed=1332055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28,
39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1864510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%;
48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakai Y., Haji M., Nawata H.; substitution (Gly743 --> Val) in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
N KINASE CATALYTIC SUBUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            androgen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65;
Pred. No.
                                                                                              SER/THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                     S.,
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648
                                                                                                                                                                                                                                                                                                                                                                     Veron M., Reymond C. CAMP-dependent prote
                                                                                              FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1:
                                                                                              OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 919;
                                                                                                                                                                                                                                       protein kinase
                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
                                                                                                                                                                                                                                                                                                                                                                     protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reifenstein
                                                                                              KINASES
                                                                                                                                                                                                                                           development,
kinase.";
                                                                                                                                                                                                                                                                                                                                                                                     .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        steroid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulated
                                        a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                    ဝှ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

the

non-profit and this st

institutions as long atement is not removed

as its content

and

d for

ij

9 ō way

```
δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation.
DOMAIN 58
DOMAIN 136
DOMAIN 233
                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the long as its 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98404153; PubMed=9732460;
Choong C.S., Kemppainen J.A., Wil
    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  disease.";
J. Mol. Evol. 47:334-342(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM: PF00433: pkinase_C; 1.
PROSITE; PS00107: PROTEIN_KINASE_ATP: 1.
PROSITE: PS00108: PROTEIN_KINASE_ST: 1.
PROSITE: PS50011: PROTEIN_KINASE_DOM: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                             "Evolution of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 097775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANDR_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR000961; -. INTERPRO; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DICTYDB; DD02030; PKAC INTERPRO; IPR000719; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR NR3C4
                                                                                                                                                                                                   DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEE
                                                                                                                                                                                                                                                                FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EURAPYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                       NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00069; pkinase; 1. PF00433; pkinase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P05132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          м38703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
12; Conserv
                                                                                                                                                                                    SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490
648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JQ1150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine-protein kinase; ATP-binding; cAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2CPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s a license agreement (S to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                           primate androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
223
250
590
350
365
459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.8%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB Pred. No. 7.7; L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASN-RICH.
GLN-RICH.
THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY).
D0F9B3A48C58D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                        receptor:
                                                                                                                                                                                                                                                                                                                                                                                                              .
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911
                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                        structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                restrictions
                                                            and
                                                                                                                  gh a collaboration EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                             basis
                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                            tor
                                                                             n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                          commercial
                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                0n
                                                                             no
                                                                           way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

```
HSP1_MOUSE
ID HSP1_MOUSE
AC PO2319
AC PO2319
DT 21-JUL
DT 21-JUL
DT 15-DEC
DE SPERM
GO MUS MU
OC EURAT)
OC MAINMAI
RN [1]
RN Kleen
RT "Nucl
RN [2]
RN EDUI
RA MEDLI
RA MEDLI
RA MEDLI
RA MEDLI
RA PEQUI
RN [3]
RN [3]
RP SEQUI
RN MEDLI
RA PEQUI
RN [4]
RP SEQUI
RN MEDLI
RA PEQUI
RI [4]
RN [4]
RN [4]
RN MEDLI
RA HECH
RN [4]
RP SEQUI
RN MEDLI
RA HECH
RN [4]
RN MEDLI
RA HECH
RN MEDLI
RA HECH
RN MEDLI
RA HECH
RN [4]
RN MEDLI
RA HECH
RN [4]
RN SEQUI
RN MEDLI
RA HECH
RN SEQUI
RN MEDLI
RA HECH
RN MEDLI
RA HECH
RN SEQUI
RN MEDLI
RN SEQUI
RN MEDLI
RA HECH
RN SEQUI
RN MEDLI
RN SEQUI
RN MEDLI
RN SEQUI
RN MEDLI
RN MEDLI
RN MEDLI
RN MEDLI
RN MEDLI
RN MEDLI
RN SEQUI
RN MEDLI
RN MEDLI
RN MEDLI
RN SEQUI
RN MEDLI
RN SEQUI
RN MEDLI
RN SEQUI
RN MEDLI
RN SEQUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88193085; PubMed=3358932;
Johnson P.A., Pschon J.J., Yelick P.C., Palm
Johnson P.A., Pschon J.J., Yelick P.C., Palm
"Sequence homologies in the mouse protamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSP1_MOUSE STANDARD; PRT; 50 AA P02319; P02319; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)
                                                                                                                                      SEQUENCE FKUM W.A.

MEDLINE=87260978; PubMed=3037541;

Peschon J.J., Behringer R.R., Brinster

Peschon J.J., Behringer R.R., Brinster

Peschon J.J., Behringer R.R., Brinster
                                                                                                                                                                                                                                                                                                                         Kleene K.C., Distel R.J., Hecht N.B.; "Nucleotide sequence of a cDNA clone Biochemistry 24:719-722(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=85199803; PubMed=2986684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Tra
Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR_RECEPTOR; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00047; STROIDFINGER. PRINTS; PR00521; ANDROGENR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00104; hormone_rec;
PFAM; PF00105; zf-C4; 1.
                                                                               SEQUENCE FROM N.A MEDLINE=88181903;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRM1 OR PRM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                nt N.B.;
ne expression
. N.Y. Acad. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEDPQTECQQCQRRCRQQESDPRQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQQQQQQQQQQQQQQQQQETSPRQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U94177; AAC73048.1; P06536; 1RGD.
                                                                                                                                Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 50.0
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001628; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000536;
IPR001103;
                                                                                                                                Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551
551
587
582
682
57
84
192
371
395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steroid-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                À
                                 Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549
616
571
611
911
98
88
196
380
401
464
98402
                                 during spermatogenesis.";
Sci. 513:90-101(1987).
                                                                                PubMed=3445973
                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                              nger R.R., Brinster R.L., Palmiter R.D.;
expression of protamine 1 in transgenic
ci. U.S.A. 84:5316-5319(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGAND-BINDING.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-PRO.
POLY-ALA.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4-TYPE
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601B9BD4E697DAA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tion update)
PROTAMINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding;
                                                                                                                                                                                                                                                                                                                                          encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                рв
10;
                                                                                                                                                                                                                                        Palmiter R.D., Hecht N.B.; mine 1 and 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                                                                                                                                                                                                          mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                        protamine 1.";
                                                                                                                                             mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

0;

```
HSP1_
                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K02926; AAA39980.1; -.
EMBL; X07625; CAA30472.1; -.
EMBL; X14003; CAA32169.1; -.
EMBL; M27500; AAA39985.1; -.
EMBL; Z47352; CAA87410.1; -.
EMBL; Z47352; CAA87410.1; -.
PIR; A02660; HSMSS1.
PIR; S03820; S03820.
                                                                                                                                                                                                                 HSP1_RAT
P10118;
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID DISULFID DISULFID
                                Klemm U., Lee C.H., Burfeind P., Hake S., Engel W.; "Nucleotide sequence of a cDNA encoding rat protamin expression of the gene during rat spermatrogenesis."; Biol. Chem. Hoppe-Seyler 370:293-301(1989).
                                                                                                                                                                 PRM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Testis; I
                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).
                                                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlueter G., Engel W.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.

1: FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPACT.

1: SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
MEDLINE=96341725;
           SEQUENCE
                                                                                     MEDLINE=89335257;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C129;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO;
                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                            6 QTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-HELIX (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                 OR PRM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A28331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:97765; PRM1.
                                                                                                                                                                                                                                                                                                      RSRCRRRRRCRR-----RRRRCCRRRRRCCRRRRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
           FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00260; protamine_P1; 1.
PS00048; PROTAMINE_P1; 1.
mal protein; Nucleosome core;
                                                                                                   FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long
                                                                                                                           Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000221; -
                                                                                                                                                                                                                                                                                                                                                                                                                             A condensation; N 0 0 0 0 5 5 5 5 6 14 21 21 21 36 36 36 37 47
                                                                                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S03820.
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Ą,
                                                                                                                                                                                                                                          STANDARD;
                                                                                   PubMed=2757789;
PubMed=8720108
                                                                                                                                                                                                                                                                                                                                                                                                                    6827
                                                                                                                                                                                                                                                                                                                                                                    25
28
                                                                                                                                                                                                                                                                                                                                                                  . 68;
                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH CYS-21) (
BY SIMILARITY,
INTERCHAIN (WITH CYS-5) (B
INTERCHAIN (WITH CYS-36) (
BY SIMILARITY,
B61CAF3D1BBF4978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                        Sciurognathi;
                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                  63.5;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions ong as its content is in
                                                            rat protamine
                                                                                                                                                                                                                                          ΑA
                                                                                                                                                                                                                                                                                                                                                                               DВ
                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                               43
                                                                                                                         Muridae;
                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYS-21) (BY
                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                           Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY
                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
L outstation -
                                                            haploid
                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   way
                                                                                                                                                                                                                                                                                                                                                       1.
```

```
В
                                                                                                                                                                                                                 δõ
                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                  DISULFID DISULFID DISULFID DISULFID DISULFID
                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upon
01-NOV-1997 (Rel. 35, Last annotation of ALLERGEN ARA H 1, CLOUE P41B (ARA H I)
                      Arachis hypogaea (Peanut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sj
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                  P43238;
01-NOV-1995
                                                                                                                           AH12_
                                                                                                                                         _ARAHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
             Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 427:752-757(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spermatozoa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlueter G., Celik A., Obata R., Sc
Schlung A., Adham I.M., Engel W.;
"Sequence analysis of the conserved
it contains a fourth expressed gene.
Mol. Reprod. Dev. 43:1-6(1996).
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 246939; CAA87061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89207111; PubMed=3072011;
                                                                                                                                                                                                                                                                                                                                                                                 INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                           restis;
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ammer H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO00221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kistler W.S., Keim P.S., Heinrikson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=76184789; PubMed=1268226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Partial structural analysis of the
                                                                                                                                                                                           11
                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-HELIX (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUNCTION: PROTAMINES SUBSTITUTES FOR HISTONESS IN THE CHROMATIN OF SPERM DURRING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DUR INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
                                                                                                                           ARAHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A27128; A27128.
S03997; S03997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a case the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sperm protamine.
. Chem. Hoppe-Sey
                                                                                                                                                                                           RSRCRRRRRCRR-----RRRRCCRRRRRCCRRRRSY
                                                                                                                                                                                                                 QTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEY
                                                                                                                                                                                                                                                                                                                                                                                                   PF00260; protamine_P1; 1.
TE; PS00048; PROTAMINE_P1; 1.
Secondal protein; Nucleosome core;
                                                                                                                                                                                                                                          l Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF 1-15 AND 44-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henschen
                                                                                                                                                                                                                                                                                                                   A condensation; N
0 0
5 5
6 14
21 21
36 36
37 47
                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoppe-Seyler
                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α.,
           Papilionoideae;
                                                                                                                                                                                                                                                                                                         6889
                                                                                                                                                                                                                                                      25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation and sequence analysis.";
ler 369:1301-1306(1988).
                                                                                                                                                                                                                                                                                                          X
X
X
                                                                                                                                                                                                                                                                                                                                                                                           Nuclear
                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WI
BY SIMILARITY.
INTERCHAIN (WI
INTERCHAIN (WI
                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                       B60B9F3D1BB6D978 CRC64;
                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                            PRT;
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                       No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlicker M., Hofferbert
             Arachis.
                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.L.; basic chromosomal protein of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protamine
                                                                                                                            626
                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                      Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions
                                                                                                                                                                                                                                                                                                                                HTIW)
                                                                                                                                                                                                                                                                                                                                             HTIW)
                                                                                                                                                                                                                                                                                                                                                                    HTIW)
                                                                                                                           A
                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                           3
                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                               CYS-5) (
                                                                                                                                                                                                                                                                                                                                                                    CYS-21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene cluster shows that
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                (BY
                                                                                                                                                                                                                                                                                                                                                                    (BY
                                                                                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                          5.
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                          ŗ
```

```
Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987
13-AUG-1987
01-NOV-1997
                                           EMBL;
PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allergen.
SEQUENCE
                                                                                                          between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAS2
                                                                                  entities requires a 
or send an email to
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                           "Complete sequence of ovine alpha s2-casein messenger RNA."; Biochimie 67:1043-1051(1985).
                                                                                                                                                                                                                                                                                      MEDLINE=86104467; PubMed=3002499;
Boisnard M., Petrissant G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                              INTERPRO; IPRO01588; -.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                  CSN1S2
                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-S2 CASEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P04654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burks A.W., Cockrell G., Stanley J.S., Helm R.M. "Recombinant peanut allergen Ara h I expression patients with peanut hypersensitivity."; J. Clin. Invest. 96:1715-1721(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96013631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-CV. FLORUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QEDPOTEC-QOCORRCROQESDPROQOYCORRCKEI 36
                                                                                                                                                                                    TISSUE SPECIFICITY: MAMMARY GLAND; MILK. SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                    SUBCELLULAR LOCATION: EXTRACELLULAR
                                                                                                                                                                                                                                 CALCIUM PHOSPHATE.
                                                                                                                                                                                                                                               FUNCTION: IMPORTANT ROLE IN THE CAPACITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO 7S SEED STORAGE PROTEINS CONVICILIN, CONGLYCININ, ETC.).
                                           ; X03238; CAA26
A25070; KASHS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKKTENPCAQRCLQSC-QQEPDDLKQKACESRCTKL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHEEP
PF00363; caseins; 2.
TE; PS00306; CASEIN_ALPHA_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L34402; AAB00861.1;
P50477; 1CAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
13; Conser
                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and this statement is not removed requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001113;
                                                                                                                                                                                                                                                                                                                                                                                    (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLORUNNER
                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 05, Created)
(Rel. 05, Last sequence update)
(Rel. 35, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                       CAA26983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7560062;
                                                                                                                                                                                                                                                                                                                                            Ovis.
                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71345 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.4%;
36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB
Pred. No. 9.5;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1A6BBBE41490D0E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helm R.M.,
                                                                                                                      There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PHASEOLIN, VICILIN
                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                             OF MILK TO TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., 'Bannon G.A.;
and IgE bindin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                           bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ру
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding
                                                                                                                                                  EMBL
                                                                                                                     ż
                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                 outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                           commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ'n
                                                                                                                      on
on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        no
                                                                                                                      way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APA4_MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                               Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APA4_MACFA P33621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
VARIANT
                                   PIR;
                                              PIR;
                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93192330; PubMed=8448212;
Osada J., Pocovi M., Nicolosi R.J.,
"Nucleotide sequences of the Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milk; |
SIGNAL
                                                          EMBL; X68361; CAA48421.1;
                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequences and A-IV genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994
15-DEC-1998
                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=LEUKOCYTE;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APOA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                              FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR COMPONENT OF HDL AND CHYLOMICRONS.
SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: SECRETED IN PLASMA.
TISSUE SPECIFICITY: SECRETED IN PLASMA.
DOMAIN: NINE OF THE THIRTEEN 27-AMINO ACID TANDEM REPEATS (EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-HELICAL, AND MANY OF THESE HELICES ARE AMPLIPATHIC. THEY MAY THEREFERDE CEDUTE AS THE TANDEM ARE AMPLIPATHIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NQEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICE--EEEEY
                                                                                                                                                                                SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY
                                                                                                                                                                                                                                                                                                                             chim. Biophys. Acta 1172:335-339(1993).
FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND
                                                                                                                                                                                           THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN: CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
                               $29565; $29565.
$30195; $30195.
                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEEPINISQEIYKQEKNMAIHPRKEKLCTTSCEEVVRNADEEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
77
159
23
24
25
72
72
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  el. 28, Created)
el. 28, Last sequence upda
el. 37, Last annotation up
a-IV PRECURSOR (APO-AIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
141
223
23
24
25
72
73
74
64
63
263
32
                                                                                            license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Crab eating macaque) (Cynomolgus monkey). Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.6%;
26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61; DB
Pred. No. 6.5;
l2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                         not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67212935E27426D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Schaefer E.J., Ordovas J.M.; fascicularis apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASEIN
                                                                                                                 There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                       γď
                                                                                                                              restrictions on i
                                                                                                       and
                                                                                                                                                      þ
                                                                                                                                                                                                                                                                                                                                                                             J.М.;
                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                           collaboration
                                                                                                                    'n
                                                                                                       commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                   C-III
                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲.
```

PF01442; Apolipoprotein;

IPR000074;

P02649;

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANDR_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Q9TT90;
30-MAY-2000
30-MAY-2000
30-MAY-2000
 DNA_BIND
ZN_FING
ZN_FING
                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
                                                Receptor; Tr
Zinc-finger;
                                                                                                                                                                                                                                                                                           androgen receptor."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasma;
SIGNAL
                                                                                  EMBL; AF197950; AAF18084.1; -
                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                         AR OR NR3C4
Canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDR_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                     DOMAIN
                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                    Molecular cloning
                                                                                                                                                                                                                                                                                                                                 Lu B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 QREQQQEQQEQEQEQQQQEQQQEQQQEQQQEQQQEQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEE 42
                                                                                                                                                                                                             DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN. A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                         FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                    NR3 SUBFAMILY.
                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                  familiaris (Dog).
vota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                Smock S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipid
                                                                        PS00031;
                                                           Transcription regulation;
; Steroid-binding.

1 545

547 612

547 567

583 607 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
33
33
60
82
115
137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                      NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                   Castleberry T.A., Owen T.A.; and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330
330
330
81
103
158
158
158
158
120
220
220
220
220
230
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
  C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.
9.
10.
11.
12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Chylomicron; Repeat; Signal.
BY SIMILARITY.
APOLIPOPROTEIN A-IV.
13 X 22 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLU/GLN-RICH
                                     MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D458F551D0DB60C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
No.

    DNA-binding; Nuclear protein;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                        907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
11;
                                    (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                    of the canine
                                                                                                                                                                   EMBL
                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,:
                                                                                                                                                                   collaboration
L outstation
                                                                                                                                                                  outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

```
δÃ
                                 Query Match
Best Local Similarity
Thes 13; Conserv
                                                                                                 RESULT 15
INVO_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990
01-NOV-1990
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVO_CANFA
P18174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                          modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                 use
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                    "The involucrin genes of pig and dog: repeats with those of prosimians and Mol. Biol. Evol. 7:293-302(1990).
                                                                                                Keratinocyte; I
SEQUENCE 285
                                                                                                                      INTERPRO; IPR002360; -.
PROSITE; PS00795; INVOLUCRIN;
                                                                                                                                            EMBL; M34442;
                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90348475; Pubmed=2385171;
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                          -i- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPE.
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO
MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE
FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE
                                                                                                                                                                                                                                                                                                                                                     Tseng H.,
                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                            INVOLUCRIN
  142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 PGAHLQQQQQQQQQQETSPRQQQQQQQ 76
                       N
                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIA.
OQQBQQBSQEKELHLEQEQQKEELQQQBQQQKEQCEKHQE
                     QEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTECOOCORRCROQESDPROQOYCOR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                 non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                     Green H.;
                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata; (
Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 16, Created)
(Rel. 16, Last seq
(Rel. 33, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678
70
70
131
180
329
375
399
                                                                                                                                            AAA30853.1;
                                                                                                             Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              (Dog).
oa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       907
64
76
134
202
332
384
                                                                                                 33384 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98726 MW;
                                                    24.2%;
31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.
                                           9;
                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-SER.
POLY-PRO.
POLY-ALA.
                                                                                                                      1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGAND-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                 DCE1BD88B9248BEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C8619F78DD2338AF CRC64;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                     NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                : comparison of their segments of
higher primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                      10;
BB (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AΑ
                                                                                                                                                                                                 as its content
                                            19;
                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 907
  182
                                                               Length 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                            Indels
                                                                                                                                                                                      bУ
                                                                                                                                                                                                          restrictions
                                                                                                                                                                                       and
                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                 a
                                           0,
                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                      collaboration -
                                                                                                                                                                                                 'n
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                      commercia.
                                                                                                                                                                                                no on
                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

Search co

completed: me: 427 sec

March

1,

2001, 16:16:47

general and a second		en de la companya de			to see s <del>e</del> see see see see	, *		
					•			
	•			the state of				
•								
•								
4								
							eri P	
	4							
-								
		**			*			
	**************************************				• .			
	* **							
		es established			•			
g., t								·
L	87							
. ;		4						
ĸi.			2.0					
					<del></del>			
			i i					
					,			
	• • • • • • • • • • • • • • • • • • • •				6			
	16.							
	•					•		
						z, .		
4 '								
						N		
						. = .		
		The second secon						2
								• .
-						•		
(s		·						
	. *				and the second s			
	•							
Te T	•		:					
'.					· · · · · · · · · · · · · · · · · · ·			
		* * * * * * * * * * * * * * * * * * *			,			
					* *			
<b>*</b>								
		•		****				
	· Vert		*					
		•						
					-			
3 1	ر میند. رامیند افزار رامیند افزار		>		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
3-4620	Service Control of		en in the contract of	* *				